10.5 PLACENTA
TESTIS
SEMINAL VESICLE
OVARY
OVIDUCT
UTERUS
BRAIN
THYMUS
HEART
LUNG
KIDNEY
ADRENAL
SPLEEN
LIVER
INTESTINE
PANCREAS

FIG. 1A

8.5
10.5
12.5
14.5
16.5
18.5

FIG. 1B

```
   1  TTCAAGCCCTCAGTCAGTTGTGCGGGAGAAAGGGGGCGGTCGGCTTTCTCCTTTCAAGAA   60
  61  CGAGTTATTTTCAGCTGCTGACTGGAGACGGTGCACGTCTGGACACGGGAGCACTTCCAC  120
 121  TATGGGACTGGATACAGACACACGCCCGGCGGACTTCAAGACACTCAGACTGAGGAGAAA  180
 181  GCCCTGCCTGCTGCTGCTGCTGCTGCTGCCACCGCTGCCTCTGAAGACCCACTCCTT    240
 241  TCATGGTTTTTCCTGCCAAGCCAGAGGCACCTTCGCTGCTACGGCCTTTCTCTGTGGTGT  300
 301  CATTCAGCGGCTGGCCAGAGGATGAGACTCCCCAAACTCCTCACTCTTTTGCTGTGGCAC  360
                              M  R  L  P  K  L  L  T  L  L  L  W  H
 361  CTGGCTTGGCTGGACCTGGAACTCATCTGCACTGTGCTGGGTGCCCCTGACTTAGGACAG  420
      L  A  W  L  D  L  E  L  I  C  T  V  L  G  A  P  D  L  G  Q
 421  AGAACCCCAGGGGCCAAGCCAGGGTTGACCAAAGCGGAGGCCAAGGAGAGGCCACCCCTG  480
      R  T  P  G  A  K  P  G  L  T  K  A  E  A  K  E  R  P  P  L
 481  GCCAGGAATGTCTTTAGGCCAGGGGGTCATATCTATGGTGTGGGGGCCACCAATGCCAGG  540
      A  R  N  V  F  R  P  G  G  H  I  Y  G  V  G  A  T  N  A  R
 541  GCCAAGGGAAGCTCTGGGCAGACACAGGCCAAGAAGGATGAACCCAGAAAGATGCCCCCC  600
      A  K  G  S  S  G  Q  T  Q  A  K  K  D  E  P  R  K  M  P  P
 601  AGATCCGGTGGCTCTGAAACCAAGCCAGGACCCTCTTCCCAGACTAGACAGGCTGCAGCC  660
      R  S  G  G  S  E  T  K  P  G  P  S  S  Q  T  R  Q  A  A  A
 661  CGGACTGTAACCCCAAAAGGACAGCTTCCTGGGGGCAAAGCATCTTCAAAAGCAGGATCT  720
      R  T  V  T  P  K  G  Q  L  P  G  G  K  A  S  S  K  A  G  S
 721  GCCCCCAGCTCCTTCCTGCTGAAGAAGACCAGGGAGCCTGGGACCCCTCGAGAGCCCAAG  780
      A  P  S  S  F  L  L  K  K  T  R  E  P  G  T  P  R  E  P  K
 781  GAGCCGTTCCGCCCGCCCCCCATCACACCCCACGAATACATGCTCTCCCTGTACAGGACG  840
      E  P  F  R  P  P  P  I  T  P  H  E  Y  M  L  S  L  Y  R  T
 841  CTGTCCGATGCTGACAGAAAGGGAGGTAACAGCAGCGTGAAGTTGGAGGCTGGCCTGGCC  900
      L  S  D  A  D  R  K  G  G  N  S  S  V  K  L  E  A  G  L  A
 901  AACACCATCACCAGCTTTATTGACAAAGGGCAAGATGACCGAGGCCCTGCGGTCAGGAAG  960
      N  T  I  T  S  F  I  D  K  G  Q  D  D  R  G  P  A  V  R  K
 961  CAGAGGTACGTGTTTGACATCAGTGCCTTGGAGAAGGATGGGCTGTTGGGGGCTGAACTG 1020
      Q  R  Y  V  F  D  I  S  A  L  E  K  D  G  L  L  G  A  E  L
1021  CGGATCTTACGGAAGAAGCCCTTGGACGTGGCCAAGCCAGCGGTCCCCAGTAGCGGGCGG 1080
      R  I  L  R  K  K  P  L  D  V  A  K  P  A  V  P  S  S  G  R
1081  GTTGCCCAACTGAAGCTGTCCAGCTGCCCCAGCGGCCGGCAGCCGGCAGCCTTGCTGGAT 1140
      V  A  Q  L  K  L  S  S  C  P  S  G  R  Q  P  A  A  L  L  D
```

FIG. 2A

```
1141  GTGCGCTCCGTGCCAGGCCTGGATGGATCTGGCTGGGAGGTGTTCGACATCTGGAAGCTC   1200
      V  R  S  V  P  G  L  D  G  S  G  W  E  V  F  D  I  W  K  L
1201  TTCCGAAATTTTAAGAACTCAGCGCAGCTGTGCCTGGAGCTGGAGGCCTGGGAACGGGGC   1260
      F  R  N  F  K  N  S  A  Q  L  C  L  E  L  E  A  W  E  R  G
1261  CGGGCCGTGGACCTCCGTGGCCTGGGCTTTGAACGCACTGCCCGACAGGTCCACGAGAAA   1320
      R  A  V  D  L  R  G  L  G  F  E  R  T  A  R  Q  V  H  E  K
1321  GCCTTGTTCCTAGTGTTTGGTCGTACCAAGAAACGGGACCTGTTCTTTAATGAGATTAAG   1380
      A  L  F  L  V  F  G  R  T  K  K  R  D  L  F  F  N  E  I  K
1381  GCCCGCTCTGGCCAGGATGACAAGACTGTGTATGAATATTTGTTCAGCCAGCGGCGGAAA   1440
      A  R  S  G  Q  D  D  K  T  V  Y  E  Y  L  F  S  Q  R  R  K
1441  CGCCGGGCCCCATTGGCCAATCGCCAGGGCAAGCGACCCAGCAAGAACCTCAAGGCTCGC   1500
      R  R  A  P  L  A  N  R  Q  G  K  R  P  S  K  N  L  K  A  R
1501  TGCAGTCGCAAGGCCTTGCATGTCAACTTCAAGGACATGGGCTGGGACGACTGGATCATC   1560
      C  S  R  K  A  L  H  V  N  F  K  D  M  G  W  D  D  W  I  I
1561  GCACCTCTTGAGTATGAGGCCTTCCACTGCGAAGGACTGTGTGAGTTCCCCTTGCGCTCC   1620
      A  P  L  E  Y  E  A  F  H  C  E  G  L  C  E  F  P  L  R  S
1621  CACTTGGAGCCCACAAACCACGCAGTCATTCAGACCCTAATGAACTCTATGGACCCTGAA   1680
      H  L  E  P  T  N  H  A  V  I  Q  T  L  M  N  S  M  D  P  E
1681  TCCACACCACCCACTTGTTGTGTGCCTACACGGCTGAGTCCTATTAGCATCCTCTTCATC   1740
      S  T  P  P  T  C  C  V  P  T  R  L  S  P  I  S  I  L  F  I
1741  GACTCTGCCAACAACGTGGTGTATAAACAGTACGAGGACATGGTCGTGGAATCTTGTGGC   1800
      D  S  A  N  N  V  V  Y  K  Q  Y  E  D  M  V  V  E  S  C  G
1801  TGCAGGTAGCAGCACCGGCCCACCTGTCTTCCAGGGTGGCACATCCAGAGACTACCCCCT   1860
      C  R  *
1861  CTACAGGTTCCTGGAGTAACAGAGAGCCTGTGAAGCTGCTGCCCGAAGTTTCCTGGCAGC   1920
1921  CTGCAGGAAAGAGTTCTCAGCAGGCTTACTCTCTGGATGTGATCTGGACTAAAGAGATCA   1980
1981  CCTTCTGAAGATTCCTGCCCAAGGAACAGACTCTGAGTGGGCCTGGGGCTCAGGAAAGGT   2040
2041  GTTCTTAATGAGATTCAGTTCACCATCTCTCCTGCCGGGGCCGGAGACCTTCATTTCTCT   2100
2101  CCAGACTCTCCAGAGAAGTTGTAGCTATATCCTAAGCTCTTTAAGGGAGAGCTGTCTCCT   2160
2161  CCTTGAATCACCTTTGTGCCTGGTGACTTTCTGCCACGAGATGTTCATTACAGGGGCTGG   2220
2221  GCAAAGAAGGGGAAAGGGCTTGGGCAGGGGTGAAGAGAAGAGTATGAGCCTAATTAGACT   2280
2281  GTTAGATTAAAATGTACATCGATGACATAAAAGCTGAATCTTCATGGCT  2329
```

FIG. 2B

```
GDF-1          RLRRHTEPRVEVGPVGTCRTRRLHVSF-REVGWHRWVIAPRGFLANFCQGTCALPETLRGPGGPP
GDF-3          RKRRAAISVPKGFCRNFCHRHQLFINF-QDLGWHKWVIAPKGFMANYCHGECPFSMTTYLNS---
GDF-5          PLANRQGKRPSKNLKARCSRKALHVNF-KDMGWDDWIIAPLEYEAFHCEGLCEFPLRSHLEP---
GDF-9          SFNLSEYFKQFLFPQNECELHDFRLSF-SQLKWDNWIVAPHRYNPRYCKGDCPRAVRHRYGS---

BMP-2          REKRQAKHKQRKRLKSSCKRHPLYVDF-SDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNS---
BMP-4          KRSPKHHSQRARKKNKNCRRHSLYVDF-SDVGWNDWIVAPPGYQAFYCHGDCPFPLADHLNS---
Vgr-1          SRGSGSSDYNGSELKTACKKHELYVSF-QDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNA---
OP-1           LRMANVAENSSSDQRQACKKHELYVSF-RDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNA---
BMP-5          SRMSSVGDYNTSEQKQACKKHELYVSF-RDLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNA---
BMP-3          EQTLKKARRKQWIEPRNCARRYLKVDF-ADIGWSEWIISPKSFDAYYCSGACQFPMPKSLKPS--
MIS            GPGRAQRSAGATAADGPCALRELSVDL----RAERSVLIPETYQANNCQGVCGWPQSDRNPRY--
Inhibin α      ALRLLQRPPEEPAAHANCHRVALNISF-QELGWERWIVYPPSFIFHYCHGGCGLHIPPNLSLPV-
Inhibin βA     HRRRRRGLECDGKV-NICCKKQFFVSF-KDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSL-
Inhibin βB     HRIRKRGLECDGRT-NLCCRQQFFIDF-RLIGWNDWIIAPTGYYGNYCEGSCPAYLAGVPGSAS-
TGF-β1         HRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWK-WIHEPKGYHANFCLGPCPYIWSLD------
TGF-β2         KKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGWK-WIHEPKGYNANFCAGACPYLWSSD------
TGF-β3         KKRALDTNYCFRNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSAD------

GDF-1          ALNHAVLRALMHA-AAPTPGAGSPCCV--PERLSPISVLFF-DNSDNVVLRHYEDMVVDECGCR
GDF-3          -SNYAFMQALMHM---ADPKVPKACCV--PTKLSPISMLYQ-DSDKNVILRHYEDMVVDECGCG
GDF-5          -TNHAVIQTLMNS--MDPESTPPTCCV--PTRLSPISILFI-DSANNVVYKQYEDMVVESCGCR
GDF-9          -PVHTMVQNIIYE--KLDPSVPRPSCV--PGKYSPLSVLTI-EPDGSIAYKEYEDMIATRCTCR

BMP-2          -TNHAIVQTLVNS---VNSKIPKACCV--PTELSAISMLYL-DENEKVVLKNYQDMVVEGCGCR
BMP-4          -TNHAIVQTLVNS---VNSSIPKACCV--PTELSAISMLYL-DEYDKVVLKNYQEMVVEGCGCR
Vgr-1          -TNHAIVQTLVHL--MNPEYVPKPCCA--PTKLNAISVLYF-DDNSNVILKKYRNMVVRACGCH
OP-1           -TNHAIVQTLVHF--INPETVPKPCCA--PTQLNAISVLYF-DDSSNVILKKYRNMVVRACGCH
BMP-5          -TNHAIVQTLVHL--MFPDHVPKPCCA--PTKLNAISVLYF-DDSSNVILKKYRNMVVRSCGCH
BMP-3          --NHATIQSIVRA-VGVVPGIPEPCCV--PEKMSSLSILFF-DENKNVVLKVYPNMTVESCACR
MIS            -GNHVVLLLKMQA--RGAALARPPCCV--PTAYAGKLLISLSEER--ISAHHVPNMVATECGCR
Inhibin α      -PGAPPTPAQPYS----LLPGAQPCCAALPGTMRPLHVRTTSDGGYSFKYETVPNLLTQHCACI
Inhibin βA     -SFHSTVINHYRMRGHSPFANLKSCCV--PTKLRPMSMLYY-DDGQNIIKKDIQNMIVEECGCS
Inhibin βB     -SFHTAVVNQYRMRGLNPGT-VNSCCI--PTKLSTMSMLYF-DDEYNIVKRDVPNMIVEECGCA
TGF-β1         -TQYSKVLALYNQ--HNPGASAAPCCV--PQALEPLPIVYY-VGRKPKV-EQLSNMIVRSCKCS
TGF-β2         -TQHSRVLSLYNT--INPEASASPCCV--SQDLEPLTILYY-IGKTPKI-EQLSNMIVKSCKCS
TGF-β3         -TTHSTVLGLYNT--LNPEASASPCCV--PQDLEPLTILYY-VGRTPKV-EQLSNMVVKSCKCS
```

FIG. 3A

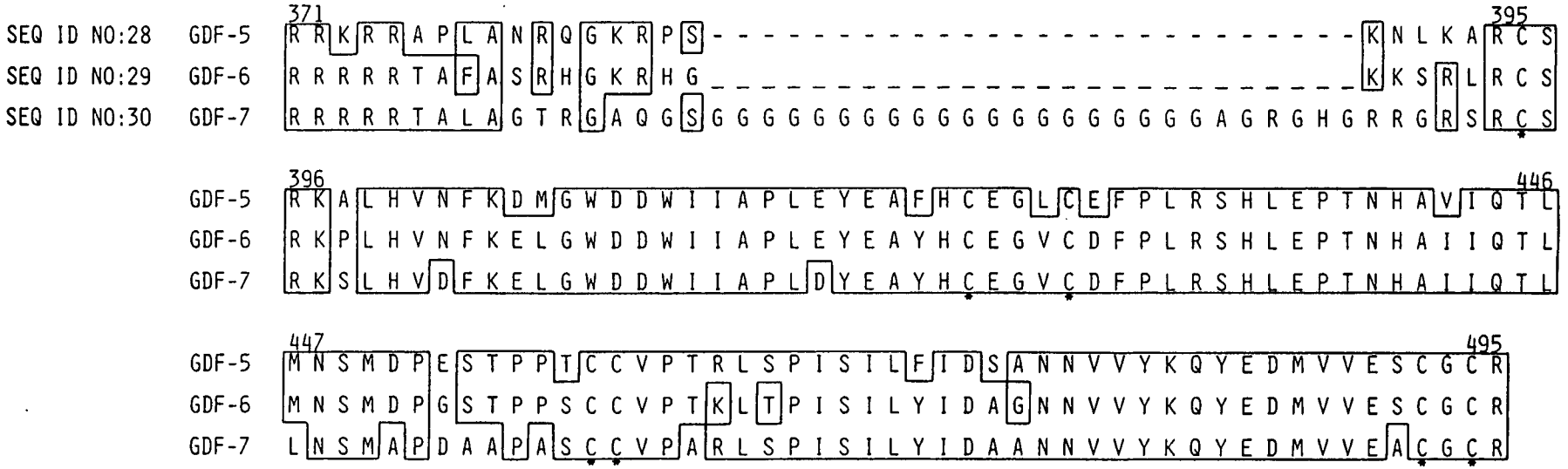

371
395
SEQ ID NO:28 GDF-5 R R K R R A P L A N R Q G K R P S - K N L K A R C S
SEQ ID NO:29 GDF-6 R R R R R T A F A S R H G K R H G _ K K S R L R C S
SEQ ID NO:30 GDF-7 R R R R R T A L A G T R G A Q G S G G G G G G G G G G G G G G G G G G G G A G R G H G R R G R S R C S
396
446
GDF-5 R K A L H V N F K D M G W D D W I I A P L E Y E A F H C E G L C E F P L R S H L E P T N H A V I Q T L
GDF-6 R K P L H V N F K E L G W D D W I I A P L E Y E A Y H C E G V C D F P L R S H L E P T N H A I I Q T L
GDF-7 R K S L H V D F K E L G W D D W I I A P L D Y E A Y H C E G V C D F P L R S H L E P T N H A I I Q T L
447
495
GDF-5 M N S M D P E S T P P T C C V P T R L S P I S I L F I D S A N N V V Y K Q Y E D M V V E S C G C R
GDF-6 M N S M D P G S T P P S C C V P T K L T P I S I L Y I D A G N N V V Y K Q Y E D M V V E S C G C R
GDF-7 L N S M A P D A A P A S C C V P A R L S P I S I L Y I D A A N N V V Y K Q Y E D M V V E A C G C R

FIG.3B

FIG. 4

	GDF-1	GDF-2	GDF-3	GDF-5	GDF-6	GDF-7	GDF-8	GDF-9	BMP-2	BMP-4	Vgr-1	OP-1	BMP-5	BMP-3	MIS	Inhibin α	Inhibin βA	Inhibin βB	TGF-β1	TGF-β2	TGF-β3
GDF-1	100	33	50	46	44	48	35	27	42	43	46	47	46	42	34	23	37	36	33	32	33
GDF-2	-	100	42	47	51	48	31	32	52	51	55	52	55	34	20	20	32	25	26	28	30
GDF-3	-	-	100	49	49	46	41	33	53	50	53	50	50	42	22	26	42	41	36	31	32
GDF-5	-	-	-	100	86	50	37	33	57	57	51	51	52	47	27	26	40	37	33	34	37
GDF-6	-	-	-	-	100	50	38	34	57	56	53	53	54	46	26	27	43	39	35	36	38
GDF-7	-	-	-	-	-	100	37	33	57	57	52	53	52	46	25	26	41	36	36	35	38
GDF-8	-	-	-	-	-	-	100	27	41	38	45	42	42	38	31	26	38	42	34	37	37
GDF-9	-	-	-	-	-	-	-	100	33	34	31	30	31	29	21	27	30	31	23	25	25
BMP-2	-	-	-	-	-	-	-	-	100	92	61	60	61	48	27	22	42	42	35	34	36
BMP-4	-	-	-	-	-	-	-	-	-	100	60	58	59	47	27	22	41	42	34	33	35
Vgr-1	-	-	-	-	-	-	-	-	-	-	100	87	91	44	24	25	44	41	35	37	39
OP-1	-	-	-	-	-	-	-	-	-	-	-	100	88	42	27	24	43	42	34	38	38
BMP-5	-	-	-	-	-	-	-	-	-	-	-	-	100	43	24	24	43	37	34	35	36
BMP-3	-	-	-	-	-	-	-	-	-	-	-	-	-	100	30	29	36	37	32	32	32
MIS	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100	18	24	25	28	23	25
Inhibin α	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100	26	25	23	22	24
Inhibin βA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100	63	41	37	36
Inhibin βB	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100	35	34	37
TGF-β1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100	74	78
TGF-β2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100	82
TGF-β3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	100

FIG. 5A



FIG. 5B

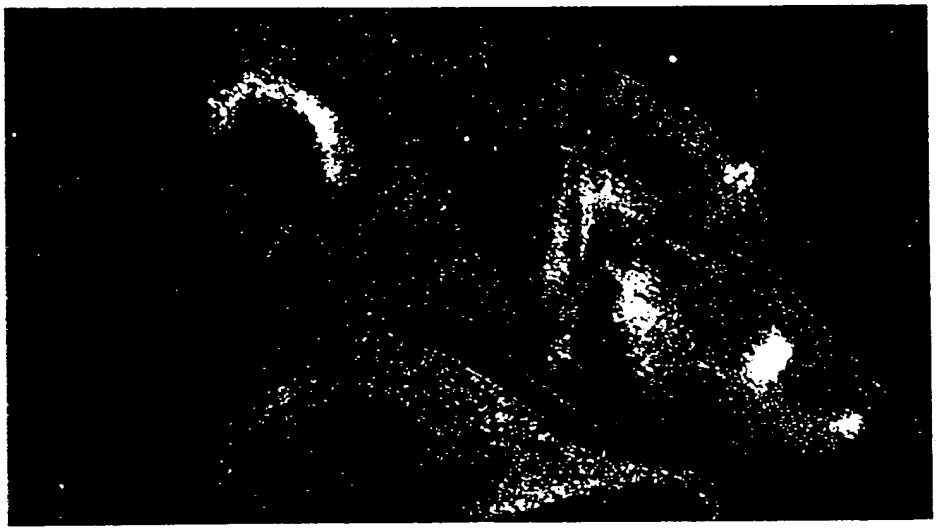


FIG. 5C

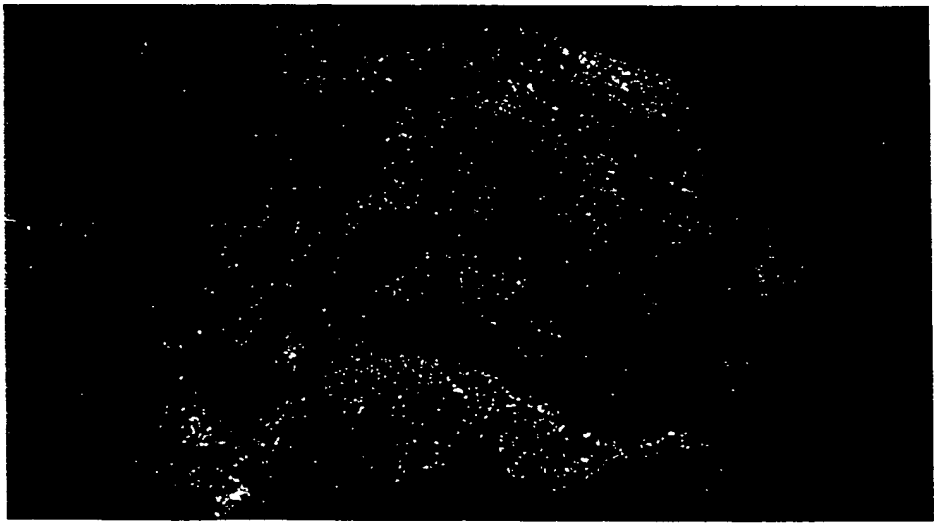


FIG. 5D

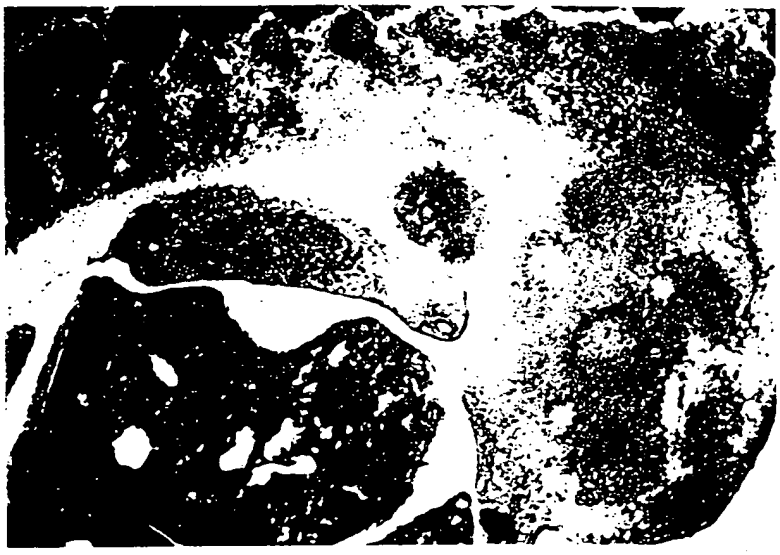


FIG. 5E



FIG. 5F

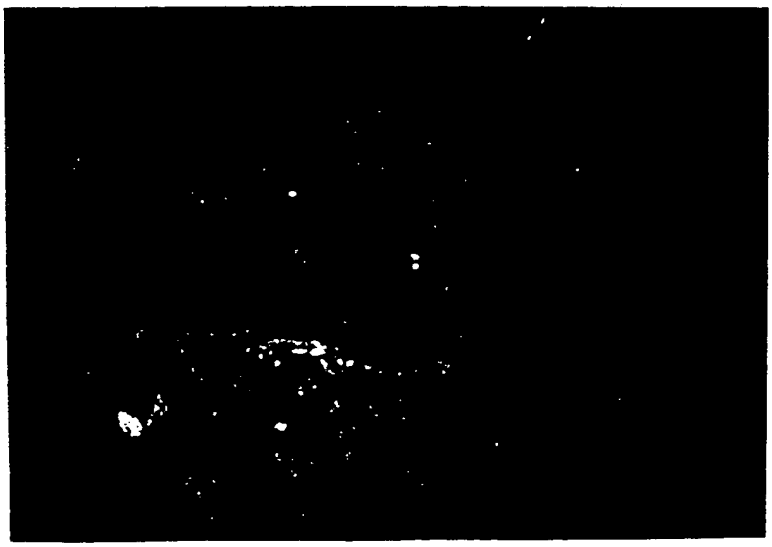




FIG. 6A

FIG. 6B



FIG. 6C